Amendments to the Specification

Please amend the specification as follows. For the convenience of the Office, deletions and insertions have been highlighted using **bold** text:

Please amend paragraph [0279] as follows:

[0279] d) ATPases Associated with Various Cellular Activities (AAA). SEQ ID NOS: 63, 116, 134, 136, 151, 384, and 404 polynucleotides encoding novel members of the "ATPases Associated with diverse cellular Activities" (AAA) protein family The AAA protein family is composed of a large number of ATPases that share a conserved region of about 220 amino acids that contains an ATP-binding site (Froehlich et al., J. Cell Biol. (1991) 114:443; Erdmann et al. Cell (1991) 64:499; Peters et al., EMBO J. (1990) 9:1757; Kunau et al., Biochimie (1993) 75:209-224; Confalonieri et al., BioEssays (1995) 17:639; ~~**http://yeamob.pci.chemie.uni-tuebingen.de/A- AA/Description.html**~~ **see internet site at yeamob.pci.chemie.uni-tuebingen.de/A- AA/Description.html**). The proteins that belong to this family either contain one or two AAA domains.

Please amend paragraph [312] as follows:

[0312] p) Trypsin. SEQ ID NO:169 corresponds to a novel serine protease of the trypsin family. The catalytic activity of the serine proteases from the trypsin family is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well conserved in this family of proteases (Brenner S., Nature (1988) 334:528). Proteases known to belong to the trypsin family include: 1) Acrosin; 2) Blood coagulation factors VII, IX, X, XI and XII, thrombin, plasminogen, and protein C; 3) Cathepsin G; 4) Chymotrypsins; 5) Complement components C1r, C1s, C2, and complement factors B, D and I; 6) Complement-activating component of RA-reactive factor; 7) Cytotoxic cell proteases (granzymes A to H); 8) Duodenase I; 9) Elastases 1, 2, 3A, 3B (protease E), leukocyte (medullasin); 10) Enterokinase (EC 3.4.21.9) (enteropeptidase); 11) Hepatocyte growth factor

activator; 12) Hepsin; 13) Glandular (tissue) kallikreins (including EGF-binding protein types A, B, and C, NGF-gamma chain, gamma-renin, prostate specific antigen (PSA) and tonin); 14) Plasma kallikrein; 15) Mast cell proteases (MCP) 1 (chymase) to 8; 16) Myeloblastin (proteinase 3) (Wegener's autoantigen); 17) Plasminogen activators (urokinase-type, and tissue-type); 18) Trypsins I, II, III, and IV; 19) Tryptases; 20) Snake venom proteases such as ancrod, batroxobin, cerastobin, flavoxobin, and protein C activator; 21) Collagenase from common cattle grub and collagenolytic protease from Atlantic sand fiddler crab; 22) Apolipoprotein(a); 23) Blood fluke cercarial protease; 24) Drosophila trypsin like proteases: alpha, easter, snake-locus; 25) Drosophila protease stubble (gene sb); and 26) Major mite fecal allergen Der p III. All the above proteins belong to family S1 in the classification of peptidases (Rawlings N. D., et al., Meth. Enzymol. (1994) 244:19; ~~http://www.expasy.ch/cgi-bin/lists?peptidas.txt~~ see worldwide web site at expasy.ch/cgi-bin/lists?peptidas.txt and originate from eukaryotic species. It should be noted that bacterial proteases that belong to family S2A are similar enough in the regions of the active site residues that they can be picked up by the same patterns.

Please amend paragraph [0360] as follows:

[0360] Homeobox domain. The `homeobox` is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homeobox Genes, Duboule D., Ed., pp1-10, Oxford University Press, Oxford, (1994); Buerglin In: Guidebook to the Homeobox Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring Trends Biochem. Sci. (1992) 17:277-280; Gehring et al Annu. Rev. Genet. (1986) 20:147-173; Schofield Trends Neurosci. (1987) 10:3-6; ~~http://copan.bioz.unibas.ch/homeo.html~~ see internet web site at copan.bioz.unibas.ch/homeo.html) first identified in number of Drosophila homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

Please amend paragraph [401] as follows:

[0401] e) ATPases Associated with Various Cellular Activities (ATPases). Several of the validation sequences, correspond to a sequence that encodes a novel member of the "ATPases Associated with diverse cellular Activities" (AAA) protein family. The AAA protein family is composed of a large number of ATPases that share a conserved region of about 220 amino acids that contains an ATP-binding site (Froehlich et al., J. Cell Biol. (1991) 114:443; Erdmann et al. Cell (1991) 64:499; Peters et al., EMBO J. (1990) 9:1757; Kunau et al., Biochimie (1993) 75:209-224; Confalonieri et al., BioEssays (1995) 17:639; ~~http://yeamob.pci.chemie.uni-tuebingen.de/A--AA/Description.html~~ **see internet site at yeamob.pci.chemie.uni-tuebingen.de/A- AA/Description.html**). The proteins that belong to this family either contain one or two AAA domains.

Please amend paragraph [0459] as follows:

[0459] All of the above proteins share a number of conserved sequence motifs. Some of them are specific to this family while others are shared by other ATP-binding proteins or by proteins belonging to the helicases `superfamily` (Hodgman T. C., Nature (1988) 333:22 and Nature (1988) 333:578 (Errata); ~~http://www.expasy.ch/www/linder/HELICASES_TEXT.html~~ **see worldwide web site at expasy.ch/www/linder/HELICASES_TEXT.html**). One of these motifs, called the `D-E-A-D-box`, represents a special version of the B motif of ATP-binding proteins. Some other proteins belong to a subfamily which have His instead of the second Asp and are thus said to be `D-E-A-H-box` proteins (Wassarman D. A., et al., Nature (1991) 349:463; Harosh I., et al., Nucleic Acids Res. (1991) 19:6331; Koonin E. V., et al., J. Gen. Virol. (1992) 73:989). Proteins currently known to belong to this DEAH subfamily are:

Please amend paragraph [0469] as follows:

[0469] r) Homeobox domain (homeobox). One SEQ ID NO, and thus the sequence it validates, represents a polynucleotide encoding a protein having a homeobox domain. The `homeobox` is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homebox Genes, Duboule D., Ed., pp1-10, Oxford University Press, Oxford, (1994); Buerglin In: Guidebook to the Homebox

Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring Trends Biochem. Sci. (1992) 17:277-280; Gehring et al Annu. Rev. Genet. (1986) 20:147-173; Schofield Trends Neurosci. (1987) 10:3-6; ~~http://copan.bioz.unibas.ch/homeo.html~~ see internet web site at copan.bioz.unibas.ch/homeo.html) first identified in number of Drosophila homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

Please amend paragraph [0474] as follows:

[0473] y) 3'5'-cyclic nucleotide phosphodiesterases signature (PDEase). One SEQ ID NO, and thus the sequence it validates, represents a polynucleotide encoding a novel 3'5'-cyclic nucleotide phosphodiesterases (PDEases). PDEases catalyze the hydrolysis of cAMP or cGMP to the corresponding nucleoside 5' monophosphates (Charbonneau H., et al, Proc. Natl. Acad. Sci. U.S.A. (1986) 83:9308). There are at least seven different subfamilies of PDEases (Beavo J. A., et al., Trends Pharmacol. Sci. (1990) 11:150; ~~http://weber.u.washington.edu/.about.pde/~~ see internet web site at weber.u.washington.edu/.about.pde/ : 1) Type 1, calmodulin/calcium-dependent PDEases; 2) Type 2, cGMP-stimulated PDEases; 3) Type 3, cGMP-inhibited PDEases; 4) Type 4, cAMP-specific PDEases; 5) Type 5, cGMP-specific PDEases; 6) Type 6, rhodopsin-sensitive cGMP-specific PDEases; and 7) Type 7, High affinity cAMP-specific PDEases.

Please amend paragraph [0509] as follows:

[0509] 7) Mammalian breast cancer type 1 susceptibility protein (BRCA1) ([E1] ~~http://bioinformatics.weizmann.ac.il/hotmolecbase/entries/brca1.htm-~~ see internet website at bioinformatics.weizmann.ac.il/hotmolecbase/entries/brca1.htm-).

Please amend paragraph [0595] as follows:

[0595] 3'5'-Cyclin Nucleotide Phosphodiesterases (PDEase). Some SEQ ID NOS represent a polynucleotide encoding a novel 3'5'-cyclic nucleotide phosphodiesterase. PDEases catalyze the hydrolysis of cAMP or cGMP to the corresponding nucleoside 5' monophosphates (Charbonneau et al, Proc. Natl. Acad. Sci. U.S.A. (1986) 83:9308). There are at least seven different subfamilies of PDEases (Beavo et al., Trends Pharmacol. Sci. (1990) 11:150; ~~http://weber.u.washington.edu/.about.pde/:~~ see internet web site at weber.u.washington.edu/.about.pde/ : 1) Type 1, calmodulin/calcium-dependent PDEases; 2) Type 2, cGMP-stimulated PDEases; 3) Type 3, cGMP-inhibited PDEases; 4) Type 4, cAMP-specific PDEases; 5) Type 5, cGMP-specific PDEases; 6) Type 6, rhodopsin-sensitive cGMP-specific PDEases; and 7) Type 7, High affinity cAMP-specific PDEases. All PDEase forms share a conserved domain of about 270 residues.

Please amend paragraph [0603] as follows:

[0603] DEAD and DEAH box families ATP-dependent helicases (Dead_box_helic). Some SEQ ID NOS represent polynucleotides encoding a novel member of the DEAD and DEAH box families (Schmid et al., Mol. Microbiol. (1992) 6:283; Linder et al., Nature (1989) 337:121; Wassarman, et al., Nature (1991) 349:463). All members of these families are involved in ATP-dependent, nucleic-acid unwinding. All DEAD box family members share a number of conserved sequence motifs, some of which are specific to the DEAD family, with others shared by other ATP-binding proteins or by proteins belonging to the helicases `superfamily` (Hodgman Nature (1988) 333:22 and Nature (1988) 333:578 (Errata); ~~http://www.expasy.ch/www/linder/HELICASES_TEXT.html~~ see worldwide web site at expasy.ch/www/linder/HELICASES_TEXT.html). One of these motifs, called the `D-E-A-D-box`, represents a special version of the B motif of ATP-binding proteins. Proteins that have His instead of the second Asp and are `D-E-A-H-box` proteins (Wassarman et al., Nature (1991) 349:463; Harosh, et al., Nucleic Acids Res. (1991) 19:6331; Koonin, et al., J. Gen. Virol. (1992) 73:989; ~~http://www.expasy.ch/www/linder/HELICASES_TEXT.html~~ see worldwide web site at expasy.ch/www/linder/HELICASES_TEXT.html).

Please amend paragraph [0720] as follows:

[0720] Helicases conserved C-terminal domain (helicase C; Pfam Accession No. PF00271). Some SEQ ID NOS represent polynucleotides encoding novel members of the DEAD/H helicase family. The DEAD box family comprises a number of eukaryotic and prokaryotic proteins involved in ATP-dependent, nucleic-acid unwinding. All DEAD box family members of the above proteins share a number of conserved sequence motifs, some of which are specific to the DEAD family while others are shared by other ATP-binding proteins or by proteins belonging to the helicases `superfamily' (Hodgman, Nature (1988) 333:22 and Nature (1988) 333:578; ~~http://www.expasy.ch/www/linder/-HELICASES_TEXT.html~~ **see worldwide web site at expasy.ch/www/linder/-HELICASES_TEXT.html**). One of these motifs, called the `D-E-A-D-box`, represents a special version of the B motif of ATP-binding proteins. Some other proteins belong to a subfamily which have His instead of the second Asp and are thus said to be `D-E-A-H-box` proteins (Wassarman D. A., et al., Nature (1991) 349:463; Harosh I., et al., Nucleic Acids Res. (1991) 19:6331; Koonin E. V., et al., J. Gen. Virol. (1992) 73:989).

Please amend paragraph [0769] as follows:

[0769] SEQ ID NOs:9920-13270 were translated in all three reading frames to determine the best alignment with the individual sequences. These amino acid sequences and nucleotide sequences are referred to, generally, as query sequences, which are aligned with the individual sequences. Query and individual sequences were aligned using the BLAST programs, available over the world wide web at ~~http://www.ncbi.nlm.nih.gov/BLAST/~~ **the web site ncbi.nlm.nih.gov/BLAST/**. Again the sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the XBLAST program for masking low complexity as described above.

Please amend paragraph [0776] as follows:

[0776] ATPases Associated with Various Cellular Activities (ATPases). Some SEQ ID NOs correspond to a sequence that encodes a novel member of the "ATPases Associated with diverse cellular Activities" (AAA) protein family. The AAA protein family is composed of a large

number of ATPases that share a conserved region of about 220 amino acids that contains an ATP-binding site (Froehlich et al., J. Cell Biol. (1991) 114:443; Erdmann et al., Cell (1991) 64:499; Peters et al., EMBO J. (1990) 9:1757; Kunau et al., Biochimie (1993) 75:209-224; Confalonieri et al., BioEssays (1995) 17:639; ~~**http://yeamob.pci.chemie.uni-tuebingen.de/AAA/Description.- html**~~ **see internet website at yeamob.pci.chemie.uni-tuebingen.de/AAA/Description.- html**). The proteins that belong to this family either contain one or two AAA domains. In general, the AAA domains in these proteins act as ATP-dependent protein clamps (Confalonieri et al. (1995) BioEssays 17:639). In addition to the ATP-binding `A` and `B` motifs, which are located in the N-terminal half of this domain, there is a highly conserved region located in the central part of the domain which was used in the development of the signature pattern.